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Letter to the Editor

Genomics, epidemiology, and common complex diseases: let's not throw out the baby with the bathwater!

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As public health professionals working to translate advances of genome-based research into population health benefits,[1,2] we found the article by Buchanan *et al.*[3] and associated commentaries[4–10] fascinating and informative. We too are sceptical of 'genohype' and we are critical of the specious paradigm that leads directly from gene discovery to test development.[11] We advocate an evidence-based approach that integrates knowledge from diverse fields—including genetic epidemiology[12]—to assess the clinical utility of genetic information for the benefit of population health.[13]

Therefore, we were astonished and disappointed to encounter Buchanan's summary dismissal of genetic epidemiology as a misguided and hopeless quest for the philosopher's stone. Delivered scarcely 3 years after completion of the Human Genome Project, this judgement is clearly premature. Population-based epidemiological research that makes the most of newly available information and techniques is just beginning. We should expect this research to take time—years, if not decades—to appropriately conduct, analyse, report, and synthesize.

Although we agree that public health programmes should continue to promote a healthy diet, adequate physical activity, and smoking cessation, it makes no sense to assert that 'the preponderance of cases of complex chronic disease are owing to exogenous experience rather than endogenous genetic susceptibility'.[10] Obviously, 'people are not born with complex, late-onset disease'; on the other hand, people who continue to eat too much, spend too much time on the couch and smoke (despite vigorous public health education campaigns) do not always develop heart disease. Clearly, there is much more to learn about gene–environment interactions underlying these diseases and to use this knowledge in intervention efforts.

As we have argued elsewhere,[14] the public health significance of genomic research on common complex diseases with strong environmental determinants lies not in finding new genetic 'causes' of these diseases but in helping us to better recognize and modify interacting environmental risk factors. Each investigation that increases our understanding of gene–environment interaction, etiological heterogeneity, pathogenesis, and natural history of common diseases adds to a knowledge base for estimating risks and guiding interventions to improve population health. Epidemiology is unique in offering a set of evolving tools and methods that are explicitly designed to observe disease variation in populations and reveal the joint effects of individual biology and behaviour in the context of social and physical environment. In an already complex world, human genetic variation is another dimension that is just now opening for exploration.[15] For epidemiologists to retreat now would be to abandon the field just when they are needed most.

The concerns enumerated by Buchanan *et al.*[3]—including phenotypic and genotypic heterogeneity, the interplay between individual and ecological variables, the dynamic nature of environmental risk, chance, and bias—are all important and well-recognized challenges in epidemiological research. Nevertheless, we take issue with their assessment that 'the lack of an obvious alternative does not justify continuing to invest in what does not work'. Indeed, there is no obvious alternative to epidemiology for translating genetic information from basic science to population health benefits but the assertion that it has not worked is simply premature. Epidemiology in the genomics era is still a baby. Let's not throw it out with the bathwater.

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